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<110> E. I. du Pont de Nemours and Company

<120> UDP-Glucose Modifiers

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<150> 60X119,588

<151> 1999-February-10

<160> 28

<170> Microsoft Office 97

<210> 1

<211> 509

<212> DNA

<213> Zea mays

<220>

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WO 00/47755

PCT/US00/03453

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 35 40 45
 Ile Asn Leu Leu Glu Val Met Ser Val His Gly Cys Lys Lys Leu Val
 50 55 60
 Phe Ser Ser Ser Ala Ala Val Tyr Gly Ser Pro Lys Asn Ser Pro Cys
 65 70 75 80
 Thr Glu Asn Phe Pro Leu Thr Pro Asn Asn Pro Tyr Gly Lys Thr Lys
 85 90 95
 Leu Val Val Glu Asp Ile Cys Arg Asp Ile Tyr Arg Ser Asp Pro Glu
 100 105 110
 Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His Pro
 115 120 125
 Ser Gly Tyr Leu Gly Glu Asp Pro Arg Xaa Ile Pro Asn Asn Leu Met
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 Leu Xaa Asn Asp Tyr Ala Thr Arg Asp
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<213> Oryza sativa

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WO 00/47755

PCT/US00/03453

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 <213> Oryza sativa

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 20 25 30
 Leu Asp Asn Ala Ser Glu Leu Ala Ile Leu Arg Val Arg Glu Leu Ala
 35 40 45
 Gly His Asn Ala Asn Asn Leu Asp Phe Arg Lys Gly Asp Leu Arg Asp
 50 55 60
 Lys Gln Ala Leu Xaa Gln Ile Phe Ser Ser Gln Lys Val Glu Xaa Val
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 Xaa Phe Tyr

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<212> DNA
<213> Glycine max

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 Ile Gly Thr His Thr Val Val Xaa Leu Leu Lys Ala Gly Phe Ser Val
 20 25 30
 Ser Ile Ile Asp Asn Phe Asp Asn Ser Val Met Glu Ala Met Asp Arg
 35 40 45

Val Arg Gln Val Val Gly Pro Leu Leu Ser Gln Asn Leu Gln Phe Thr
 50 55 60

Gln Gly Asp Leu Arg Asn Arg Asp Asp Leu Glu Lys Leu Phe Ser Lys
 65 70 75 80

Thr Thr Phe Asp Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Ala
 85 90 95

Glu Ser Val Ala Lys Pro Arg Arg Tyr Phe Asp Phe Asn Leu Xaa Gly
 100 105 110

Thr Xaa Asn Leu Tyr Glu Phe Met Xaa Lys Tyr Asn Cys Lys Lys Met
 115 120 125

Gly Phe Ser Ser Ser Ala Thr Val Tyr Gly Gln Xaa Glu Lys Ile Pro
 130 135 140

Cys Glu Glu Asp
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 <213> Triticum aestivum

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 <211> 162
 <212> PRT
 <213> Triticum aestivum

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 Asn Ser Val Pro Glu Ala Leu Asp Arg Val Arg His Ile Val Gly Pro
 35 40 45
 Ala Leu Ser Ala Arg Leu Gln Phe Ile Phe Gly Asp Leu Thr Ile Lys
 50 55 60
 Asp Asp Leu Glu Lys Val Phe Ala Ala Lys Lys Tyr Asp Ala Val Ile
 65 70 75 80
 His Phe Ala Gly Leu Lys Ala Val Ala Glu Ser Val Ala His Pro Glu
 85 90 95
 Met Tyr Asn Arg Asn Asn Ile Val Gly Thr Val Asn Leu Tyr Asp Val
 100 105 110
 Met Lys Lys His Gly Cys Asn Lys Leu Val Phe Ser Ser Ser Ala Thr
 115 120 125
 Val Tyr Gly Gln Pro Glu Lys Val Pro Cys Phe Glu Asp Ser Pro Leu
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 Lys Ala Leu Asn Pro Tyr Gly Arg Thr Lys Leu Tyr Trp Arg Arg Ser
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Ala Arg

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WO 00/47755

PCT/US00/03453

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<222> (196)..(197)

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Ala His Pro Glu Met Tyr Tyr Glu Asn Asn Leu Ile Gly Thr Ile Asn
 20 25 30

Leu Tyr Lys Ser Met Lys Glu His Gly Cys Lys Lys Leu Val Phe Ser
 35 40 45

Ser Ser Ala Thr Val Tyr Gly Trp Pro Glu Val Ile Pro Cys Val Glu
 50 55 60

Asp Ser Lys Leu Gln Ala Ala Asn Pro Tyr Gly Arg Thr Lys Leu Ile
 65 70 75 80

Leu Glu Asp Met Ala Arg Asp Tyr His Arg Ala Asp Thr Glu Trp Ser
 85 90 95

Ile Val Leu Leu Arg Tyr Phe Asn Pro Ile Gly Ala His Ser Ser Gly
 100 105 110

Xaa Ile Xaa Arg Gly Pro Gln Gly Asp Thr Glu Gln Pro Ala Ala Leu
 115 120 125

His Pro Ala Gly Xaa Arg Arg Xaa Ala Pro Arg Ala Gln Arg Leu Arg
 130 135 140

Xaa Thr Ile Thr Pro Pro Gly Asp Gly Thr Ala Ile Arg Asp Tyr Ile
 145 150 155 160

His Val Val Glu Leu Ala Asp Gly His Ile Ala Arg Ala Xaa Glu Leu
 165 170 175

Xaa Asp Ser Pro Asp Ile Ser Cys Val Gly Tyr Asn Leu Gly Val Gln
 180 185 190

Gly Arg Arg Xaa Xaa
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<213> Oryza sativa

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 <213> Oryza sativa

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 20 25 30

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Ser Arg Asn Pro Gln Met Tyr Tyr Glu Asp Asn Val Ala Gly Thr Met
 35 40 45

Asn Leu Xaa Ser Ala Leu Thr Lys Tyr Gly Xaa Xaa Xaa Ile Val Phe
 50 55 60

Ser Ser Xaa Ala Thr Val Xaa Gly Gln Pro Xaa Lys Thr Pro Cys Val
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Glu Xaa Ser Xaa Leu Ser Ala Leu Asn Pro Tyr Gly Ala Xaa Xaa Leu
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Val Leu Glu

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<400> 14

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			20					25					30		

Ser	Ile	Ile	Asp	Asn	Phe	Asp	Asn	Ser	Val	Met	Glu	Ala	Val	Asp	Arg
			35				40					45			

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Val Arg Gln Val Val Gly Pro Leu Leu Ser Gln Asn Leu Gln Phe Thr
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 Gln Gly Asp Leu Arg Asn Arg Asp Asp Leu Glu Lys Leu Phe Ser Lys
 65 70 75 80
 Thr Thr Phe Asp Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Ala
 85 90 95
 Glu Ser Val Ala Lys Pro Arg Arg Tyr Phe Asp Phe Asn Leu Val Gly
 100 105 110
 Thr Ile Asn Leu Tyr Glu Phe Met Ala Lys Tyr Asn Cys Lys Lys Met
 115 120 125
 Val Phe Ser Ser Ser Ala Thr Val Tyr Gly Gln Pro Glu Lys Ile Pro
 130 135 140
 Cys Glu Glu Asp Phe Lys Leu Gln Ala Met Asn Pro Tyr Gly Arg Thr
 145 150 155 160
 Lys Leu Phe Leu Glu Glu Ile Ala Arg Asp Ile Gln Lys Ala Glu Pro
 165 170 175
 Glu Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His
 180 185 190
 Glu Ser Gly Lys Leu Gly Glu Asp Pro Lys Gly Ile Pro Asn Asn Leu
 195 200 205
 Met Pro Tyr Ile Gln Gln Val Ala Val Gly Arg Leu Thr Glu Leu Asn
 210 215 220
 Val Tyr Gly His Asp Tyr Pro Thr Arg Asp Gly Ser Ala Ile Arg Asp
 225 230 235 240
 Tyr Ile His Val Met Asp Leu Ala Asp Gly His Ile Ala Ala Leu Arg
 245 250 255
 Lys Leu Phe Thr Thr Glu Asn Ile Gly Cys Thr Ala Tyr Asn Leu Gly
 260 265 270
 Thr Gly Arg Gly Thr Ser Val Leu Glu Met Val Thr Ala Phe Glu Lys
 275 280 285
 Ala Ser Gly Lys Lys Ile Pro Val Lys Leu Cys Pro Arg Arg Pro Gly
 290 295 300
 Asp Ala Thr Glu Val Tyr Ala Ser Thr Glu Arg Ala Glu Lys Glu Leu
 305 310 315 320
 Gly Trp Lys Ala Asn Tyr Gly Val Glu Glu Met Cys Arg Asp Gln Trp
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<210> 15
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WO 00/47755

PCT/US00/03453

<212> DNA
 <213> Triticum aestivum

<220>
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 <222> (1458)..(1459)

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<210> 16
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 <212> PRT
 <213> Triticum aestivum

<400> 16
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 His Thr Val Leu Gln Leu Leu Glu Lys Gly Tyr Ala Val Thr Ala Val
 20 25 30
 Asp Asn Phe His Asn Ser Val Pro Glu Ala Leu Asp Arg Val Arg His
 35 40 45
 Ile Val Gly Pro Ala Leu Ser Ala Arg Leu Gln Phe Ile Phe Gly Asp
 50 55 60
 Leu Thr Ile Lys Asp Asp Leu Glu Lys Val Phe Ala Ala Lys Lys Tyr
 65 70 75 80
 Asp Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Ala Glu Ser Val
 85 90 95

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Ala His Pro Glu Met Tyr Asn Arg Asn Asn Ile Val Gly Thr Val Asn
100 105 110

Leu Tyr Asp Val Met Lys Lys His Gly Cys Asn Lys Leu Val Phe Ser
115 120 125

Ser Ser Ala Thr Val Tyr Gly Gln Pro Glu Lys Val Pro Cys Phe Glu
130 135 140

Asp Ser Pro Leu Lys Ala Leu Asn Pro Tyr Gly Arg Thr Lys Leu Tyr
145 150 155 160

Leu Glu Glu Met Leu Arg Asp Tyr Gln His Ala Asn Pro Glu Trp Arg
165 170 175

Thr Ile Leu Leu Arg Tyr Phe Asn Pro Ile Gly Ala His Glu Ser Gly
180 185 190

Asp Ile Gly Glu Asp Pro Lys Gly Val Pro Asn Asn Leu Leu Pro Tyr
195 200 205

Ile Gln Gln Val Ala Val Ala Arg Arg Pro Glu Leu Asn Val Tyr Gly
210 215 220

His Asp Tyr Arg Thr Arg Asp Gly Thr Ala Val Arg Asp Tyr Ile His
225 230 235 240

Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Glu Lys Leu Phe
245 250 255

Ala Thr Pro Asp Ile Gly Cys Val Ala Tyr Asn Leu Gly Thr Gly Arg
260 265 270

Gly Thr Thr Val Leu Glu Met Val Ser Ala Phe Glu Lys Ala Tyr Gly
275 280 285

Lys Lys Ile Pro Val Lys Met Cys Pro Arg Arg Pro Gly Asp Ser Glu
290 295 300

Gln Val Tyr Ala Ser Thr Ala Lys Ala Glu Glu Glu Leu Gly Trp Arg
305 310 315 320

Ala Lys Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn Trp Ala
325 330 335

Lys Lys Asn Pro Tyr Gly Tyr Cys Gly Asn Ala Ala Glu Asn Lys Asp
340 345 350

<210> 17
<211> 1393
<212> DNA
<213> Zea mays

<400> 17
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ttgaagctgt cattcacttc gctggattga aagctgtggg tgaaagcgta cagaagccat 120
tactttatta tgacaacaac gtcattggca cgataaatct tctagaagtt atgtctgttc 180
acggttgcaa gaagttgggtg ttctcatcat cagctgcagt ttatggatca cccaaaaact 240
caccctgcac agaaaatttt cctcttactc caaacaatcc atatggcaaa acaaagctcg 300
ttgttgaaga tatttgccgg gatattctacc gttcagatcc tgaatggaag atcattttac 360

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ttaggtactt caatccagtt ggtgctcatc ctagtgata tcttgccgag gacccacgag 420
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taacagtttt aggaaatgac tatgcaacaa gagatgggac tgggggccga gattacatcc 540
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gcatagggtg tgaagcgtac aaccttgaa ccggaagagg tacatctgtg ctggagattg 660
ttaaagcatt tgagaaggct tctgggaaga aaatacctct gatttttggg gaaagacgcc 720
caggtgatgc agagattctg ttttcagaga ctactaaagc agagagggag cttaactgga 780
aagcaaaata cgggtattgaa gagatgtgcc gcgaccaatg gaactgggcc agcaagaacc 840
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gatcatcaga cctcaagccg aatggtaatg gccacctgcg ctgagcagaa ctggttgccc 1080
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aaaaaaaaaa aaa 1393

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<210> 18
 <211> 353
 <212> PRT
 <213> Zea mays

<400> 18
 Thr Arg Ile Asp Leu Arg Asp Lys Gly Ala Leu Glu Met Val Phe Ala
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 Ser Thr Arg Phe Glu Ala Val Ile His Phe Ala Gly Leu Lys Ala Val
 20 25 30
 Gly Glu Ser Val Gln Lys Pro Leu Tyr Tyr Asp Asn Asn Val Ile
 35 40 45
 Gly Thr Ile Asn Leu Leu Glu Val Met Ser Val His Gly Cys Lys Lys
 50 55 60
 Leu Val Phe Ser Ser Ser Ala Ala Val Tyr Gly Ser Pro Lys Asn Ser
 65 70 75 80
 Pro Cys Thr Glu Asn Phe Pro Leu Thr Pro Asn Asn Pro Tyr Gly Lys
 85 90 95
 Thr Lys Leu Val Val Glu Asp Ile Cys Arg Asp Ile Tyr Arg Ser Asp
 100 105 110
 Pro Glu Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala
 115 120 125
 His Pro Ser Gly Tyr Leu Gly Glu Asp Pro Arg Gly Ile Pro Asn Asn
 130 135 140
 Leu Met Pro Tyr Val Gln Gln Val Ala Val Gly Arg Arg Pro Ala Leu
 145 150 155 160
 Thr Val Leu Gly Asn Asp Tyr Ala Thr Arg Asp Gly Thr Gly Val Arg
 165 170 175
 Asp Tyr Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu
 180 185 190

Gln Lys Leu Phe Glu Asn Ser Ser Ile Gly Cys Glu Ala Tyr Asn Leu
 195 200 205

Gly Thr Gly Arg Gly Thr Ser Val Leu Glu Ile Val Lys Ala Phe Glu
 210 215 220

Lys Ala Ser Gly Lys Lys Ile Pro Leu Ile Phe Gly Glu Arg Arg Pro
 225 230 235 240

Gly Asp Ala Glu Ile Leu Phe Ser Glu Thr Thr Lys Ala Glu Arg Glu
 245 250 255

Leu Asn Trp Lys Ala Lys Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln
 260 265 270

Trp Asn Trp Ala Ser Lys Asn Pro Tyr Gly Tyr Gly Ser Pro Asp Ser
 275 280 285

Ile Lys Gln Asn Gly His Gln Thr Asn Gly Ser Ala Asp Ser Ser Lys
 290 295 300

Gln Asn Gly His Arg Thr Asn Gly Ser Thr Asp Ser Pro Lys Arg Asn
 305 310 315 320

Gly His His Ala Tyr Gly Ser Ala Asp Ser Pro Lys Arg Asn Gly His
 325 330 335

Cys Val Phe Gly Ser Ser Asp Leu Lys Pro Asn Gly Asn Gly His Leu
 340 345 350

Arg

<210> 19
 <211> 1498
 <212> DNA
 <213> Oryza sativa

<400> 19
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 cacacacgca cacaacaaca acaagagtaa tcaaagtaga agaagatggt ttcggccttg 120
 ttgcggaagc tcttggtgac gggcggcgcc ggctacatcg gcagccacac cgtcctccag 180
 cttctccaac tcggcttccg cgttgctcgtc ctcgacaacc tcgacaacgc ctccgagctc 240
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 gtcattccatt ttgccgggct gaaagctggt ggcgagagcg tgcagaagcc cctgctttac 420
 tacgacaaca acctcatcgg caccatcact ctcttcgagg tcatggccgc acatggctgc 480
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 gatctagcgg atggtcatat cgccgcgtta aggaagctct atgaagattc tgatagaata 900
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 gcattcgaga aagcttctgg aaagaaaatc ccgcttgat ttgctggacg aaggcctgga 1020
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gtagcagcag cagcagcatg acttctatac atatatatat ataatacataa agaatagaaga 1260
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 cctctaatat aatctccata tttatggtag aaataaattt tgcccaccgt ggaagaacta 1440
 tataatagaa tcatgatgat ttgttgatta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1498

<210> 20
 <211> 354
 <212> PRT
 <213> Oryza sativa

<400> 20

Met Val Ser Ala Leu Leu Arg Thr Ile Leu Val Thr Gly Gly Ala Gly
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Tyr Ile Gly Ser His Thr Val Leu Gln Leu Leu Gln Leu Gly Phe Arg
 20 25 30

Val Val Val Leu Asp Asn Leu Asp Asn Ala Ser Glu Leu Ala Ile Leu
 35 40 45

Arg Val Arg Glu Leu Ala Gly His Asn Ala Asn Asn Leu Asp Phe Arg
 50 55 60

Lys Val Asp Leu Arg Asp Lys Gln Ala Leu Asp Gln Ile Phe Ser Ser
 65 70 75 80

Gln Arg Phe Glu Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Gly
 85 90 95

Glu Ser Val Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn Leu Ile Gly
 100 105 110

Thr Ile Thr Leu Leu Gln Val Met Ala Ala His Gly Cys Thr Lys Leu
 115 120 125

Val Phe Ser Ser Ser Ala Thr Val Tyr Gly Trp Pro Lys Glu Val Pro
 130 135 140

Cys Thr Glu Glu Ser Pro Leu Cys Ala Met Asn Pro Tyr Gly Arg Thr
 145 150 155 160

Lys Leu Val Ile Glu Asp Met Cys Arg Asp Leu His Ala Ser Asp Pro
 165 170 175

Asn Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His
 180 185 190

Pro Ser Gly Tyr Ile Gly Glu Asp Pro Cys Gly Ile Pro Asn Asn Leu
 195 200 205

Met Pro Phe Val Gln Gln Val Ala Val Gly Arg Arg Pro Ala Leu Thr
 210 215 220

Val Tyr Gly Thr Asp Tyr Asn Thr Lys Asp Gly Thr Gly Val Arg Asp
 225 230 235 240

Tyr Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Arg
 245 250 255

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Lys Leu Tyr Glu Asp Ser Asp Arg Ile Gly Cys Glu Val Tyr Asn Leu
 260 265 270
 Gly Thr Gly Lys Gly Thr Ser Val Leu Glu Met Val Ala Ala Phe Glu
 275 280 285
 Lys Ala Ser Gly Lys Lys Ile Pro Leu Val Phe Ala Gly Arg Arg Pro
 290 295 300
 Gly Asp Ala Glu Ile Val Tyr Ala Gln Thr Ala Lys Ala Glu Lys Glu
 305 310 315 320
 Leu Lys Trp Lys Ala Lys Tyr Gly Val Glu Glu Met Cys Arg Asp Leu
 325 330 335
 Trp Asn Trp Ala Ser Lys Asn Pro Tyr Gly Tyr Gly Ser Pro Asp Ser
 340 345 350

Ser Asn

<210> 21
 <211> 1532
 <212> DNA
 <213> Glycine max

<400> 21
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 ccgaatatgg catcgcgctg cagcattggc aaccttacct cctccgcgcc gtatatataat 120
 tccccctact ttcgctcacc acttaagatt tccaacaacc cctctctgca aaacgcttcg 180
 cataaggtac ttatgcgcga taagactgta ctggtaaccg gcggagccgg ttacatcggc 240
 agccacaccg ttcttcagct cttgctcgga ggtttcagag ccgtcgtcct cgacaacctc 300
 gaaaattcct ccgaggttgc catccacaga gtcagggagc tcgccggcga atttgggaac 360
 aacctctcct ttcacaaggt ggacctacgg gacagagctg ctctagacca aatattttct 420
 tccacacaat tcgatgctgt catacatttt gctggactga aagcagtagg agaaagtgtg 480
 caaaaacctt tactatacta taacaacaac ttgactggga caatcactct attggaagtc 540
 atggctgccc atggatgcaa gaagctcgtg ttttcatctt cagcaactgt atatggttgg 600
 ccaaaggagg ttccatgcac agaagagttc cctctgtcag caatgaacct atatggacga 660
 actaagctta tcattgaaga aatttgccgt gatgtccact gtgcagagcc agattgtaaa 720
 ataattttgt taagatactt caaccaggtt ggtgcacacc ccagtgggta tattggggag 780
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 gaacctaaata taggttggtga ggtttataac ctgggaacag gaaaggaac atcagttttg 1020
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 aaaaacctt atggctatgg agatcagggc tccaccgatt aaccacttag ttttctcttt 1260
 gggttctttt ctgaactcac ccacaccgta gtccgtaggt cttgtgaatt tagttttccc 1320
 aaaagctttt ctttctttag tgatcttaag gtgacaaagt acttgattta ttactattca 1380
 tagttacata gtaagtaagt agtggtttac tatactgtaa tttaaagggt ctctagggtc 1440
 cttcttacag gttattgatt attagattcg gattctctca tgttccacat gagcagcate 1500
 ctgttttgta aatctaaatc acatgtttgt tt 1532

<210> 22
 <211> 349
 <212> PRT
 <213> Glycine max

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<400> 22

Met Arg Asp Lys Thr Val Leu Val Thr Gly Gly Ala Gly Tyr Ile Gly
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Ser His Thr Val Leu Gln Leu Leu Leu Gly Gly Phe Arg Ala Val Val
 20 25 30

Leu Asp Asn Leu Glu Asn Ser Ser Glu Val Ala Ile His Arg Val Arg
 35 40 45

Glu Leu Ala Gly Glu Phe Gly Asn Asn Leu Ser Phe His Lys Val Asp
 50 55 60

Leu Arg Asp Arg Ala Ala Leu Asp Gln Ile Phe Ser Ser Thr Gln Phe
 65 70 75 80

Asp Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Val
 85 90 95

Gln Lys Pro Leu Leu Tyr Tyr Asn Asn Asn Leu Thr Gly Thr Ile Thr
 100 105 110

Leu Leu Glu Val Met Ala Ala His Gly Cys Lys Lys Leu Val Phe Ser
 115 120 125

Ser Ser Ala Thr Val Tyr Gly Trp Pro Lys Glu Val Pro Cys Thr Glu
 130 135 140

Glu Phe Pro Leu Ser Ala Met Asn Pro Tyr Gly Arg Thr Lys Leu Ile
 145 150 155 160

Ile Glu Glu Ile Cys Arg Asp Val His Cys Ala Glu Pro Asp Cys Lys
 165 170 175

Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His Pro Ser Gly
 180 185 190

Tyr Ile Gly Glu Asp Pro Arg Gly Ile Pro Asn Asn Leu Met Pro Phe
 195 200 205

Val Gln Gln Val Ala Val Gly Arg Arg Pro Ala Leu Thr Val Phe Gly
 210 215 220

Asn Asp Tyr Asn Thr Ser Asp Gly Thr Gly Val Arg Asp Tyr Ile His
 225 230 235 240

Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Leu Lys Leu Asp
 245 250 255

Glu Pro Asn Ile Gly Cys Glu Val Tyr Asn Leu Gly Thr Gly Lys Gly
 260 265 270

Thr Ser Val Leu Glu Met Val Arg Ala Phe Glu Met Ala Ser Gly Lys
 275 280 285

Lys Ile Pro Leu Val Met Ala Gly Arg Arg Pro Gly Asp Ala Glu Ile
 290 295 300

Val Tyr Ala Ser Thr Lys Lys Ala Glu Arg Glu Leu Lys Trp Lys Ala
 305 310 315 320

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Lys Tyr Gly Ile Asp Glu Met Cys Arg Asp Gln Trp Asn Trp Ala Ser
 325 330 335

Lys Asn Pro Tyr Gly Tyr Gly Asp Gln Gly Ser Thr Asp
 340 345

<210> 23
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 <212> DNA
 <213> Triticum aestivum

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WO 00/47755

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<220>
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 <221> unsure
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 <221> unsure
 <222> (482)

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 ttccgcgtcc tcgtagtcga cagcctcgac aacgcctccg aggaggccat ccgccgcgtc 180
 cgacaactcg ccaacgcccc gcaaaanagc ctcgacttcc gcaagggtga ccttcgtgac 240
 aaggangcgc tcgaccaaatt cttctcctcc caaagggtatc ttcnactttt ttccgcaaaa 300
 aagaagtatc ttttttcgng cttattatta anaattaact atagtatatt attgagtcca 360
 caaattaaat gttgattntt cegtccgtcc cggccgtcgt gccagccanc canccgtntc 420
 tgctgctata gcaaatacga ctcttttcta tcagnatcgt ngtcgttngt aggtgtcaan 480
 cncctacgag 490

<210> 24
 <211> 103
 <212> PRT
 <213> Triticum aestivum

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 <222> (74)

<220>
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<220>

<221> UNSURE

<222> (90)

<400> 24

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Leu Gln Gly Phe Arg Val Leu Val Val Asp Ser Leu Asp Asn Ala Ser
 20 25 30

Glu Glu Ala Ile Arg Arg Val Arg Gln Leu Ala Asn Ala Pro Gln Xaa
 35 40 45

Ser Leu Asp Phe Arg Lys Val Asp Leu Arg Asp Lys Xaa Ala Leu Asp
 50 55 60

Gln Ile Phe Ser Ser Gln Arg Tyr Leu Xaa Leu Phe Ser Ala Lys Lys
 65 70 75 80

Lys Tyr Leu Phe Ser Xaa Leu Leu Leu Xaa Ile Asn Tyr Ser Ile Leu
 85 90 95

Leu Ser Pro Gln Ile Lys Cys
 100

<210> 25

<211> 350

<212> PRT

<213> Pisum sativum

<400> 25

Met Val Ala Ser Ser Gln Lys Ile Leu Val Thr Gly Ser Ala Gly Phe
 1 5 10 15

Ile Gly Thr His Thr Val Val Gln Leu Leu Asn Asn Gly Phe Asn Val
 20 25 30

Ser Ile Ile Asp Asn Phe Asp Asn Ser Val Met Glu Ala Val Glu Arg
 35 40 45

Val Arg Glu Val Val Gly Ser Asn Leu Ser Gln Asn Leu Glu Phe Thr
 50 55 60

Leu Gly Asp Leu Arg Asn Lys Asp Asp Leu Glu Lys Leu Phe Ser Lys
 65 70 75 80

Ser Lys Phe Asp Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Gly
 85 90 95

Glu Ser Val Glu Asn Pro Arg Arg Tyr Phe Asp Asn Asn Leu Val Gly
 100 105 110

Thr Ile Asn Leu Tyr Glu Val Met Ala Lys His Asn Cys Lys Lys Met
 115 120 125

Val Phe Ser Ser Ser Ala Thr Val Tyr Gly Gln Pro Glu Lys Ile Pro
 130 135 140

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Cys Val Glu Asp Phe Lys Leu Gln Ala Met Asn Pro Tyr Gly Arg Thr
 145 150 155 160
 Lys Leu Phe Leu Glu Glu Ile Ala Arg Asp Ile Gln Lys Ala Glu Pro
 165 170 175
 Glu Trp Arg Ile Val Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His
 180 185 190
 Glu Ser Gly Lys Leu Gly Glu Asp Pro Arg Gly Ile Pro Asn Asn Leu
 195 200 205
 Met Pro Tyr Ile Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu Asn
 210 215 220
 Val Tyr Gly His Asp Tyr Pro Thr Arg Asp Gly Ser Ala Ile Arg Asp
 225 230 235 240
 Tyr Ile His Val Met Asp Leu Ala Asp Gly His Ile Ala Ala Leu Arg
 245 250 255
 Lys Leu Phe Thr Ser Glu Asn Ile Gly Cys Thr Ala Tyr Asn Leu Gly
 260 265 270
 Thr Gly Arg Gly Ser Ser Val Leu Glu Met Val Ala Ala Phe Glu Lys
 275 280 285
 Ala Ser Gly Lys Lys Ile Ala Leu Lys Leu Cys Pro Arg Arg Pro Gly
 290 295 300
 Asp Ala Thr Glu Val Tyr Ala Ser Thr Ala Lys Ala Glu Lys Glu Leu
 305 310 315 320
 Gly Trp Lys Ala Lys Tyr Gly Val Glu Glu Met Cys Arg Asp Gln Trp
 325 330 335
 Asn Trp Ala Lys Asn Asn Pro Trp Gly Tyr Ser Gly Lys Pro
 340 345 350
 <210> 26
 <211> 350
 <212> PRT
 <213> Cyamopsis tetragonoloba
 <400> 26
 Met Ser Ser Gln Thr Val Leu Val Thr Gly Gly Ala Gly Tyr Ile Gly
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 Ser His Thr Val Leu Gln Leu Leu Leu Gly Gly Phe Lys Ala Val Val
 20 25 30
 Val Asp Asn Leu Asp Asn Ser Ser Glu Thr Ala Ile His Arg Val Lys
 35 40 45
 Glu Leu Ala Gly Lys Phe Ala Gly Asn Leu Ser Phe His Lys Leu Asp
 50 55 60
 Leu Arg Asp Arg Asp Ala Leu Glu Lys Ile Phe Ser Ser Thr Lys Phe
 65 70 75 80

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Asp Ser Val Ile His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Val
 85 90 95
 Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn Leu Ile Gly Thr Ile Val
 100 105 110
 Leu Phe Glu Val Met Ala Ala His Gly Cys Lys Lys Leu Val Phe Ser
 115 120 125
 Ser Ser Ala Thr Val Tyr Gly Leu Pro Lys Glu Val Pro Cys Thr Glu
 130 135 140
 Glu Phe Pro Leu Ser Ala Ala Asn Pro Tyr Gly Arg Thr Lys Leu Ile
 145 150 155 160
 Ile Glu Glu Ile Cys Arg Asp Ile Tyr Arg Ala Glu Gln Glu Trp Lys
 165 170 175
 Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His Pro Ser Gly
 180 185 190
 Tyr Ile Gly Glu Asp Pro Arg Gly Ile Pro Asn Asn Leu Met Pro Phe
 195 200 205
 Val Gln Gln Val Ala Val Gly Arg Arg Pro Ala Leu Thr Val Phe Gly
 210 215 220
 Asn Asp Tyr Thr Thr Ser Asp Gly Thr Gly Val Arg Asp Tyr Ile His
 225 230 235 240
 Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Arg Lys Leu Asn
 245 250 255
 Asp Pro Lys Ile Gly Cys Glu Val Tyr Asn Leu Gly Thr Gly Lys Gly
 260 265 270
 Thr Ser Val Leu Glu Met Val Lys Ala Phe Glu Gln Ala Ser Gly Lys
 275 280 285
 Lys Ile Pro Leu Val Met Ala Gly Arg Arg Pro Gly Asp Ala Glu Val
 290 295 300
 Val Tyr Ala Ser Thr Asn Lys Ala Glu Arg Glu Leu Asn Trp Lys Ala
 305 310 315 320
 Lys Tyr Gly Ile Asp Glu Met Cys Arg Asp Gln Trp Asn Trp Ala Ser
 325 330 335
 Lys Asn Pro Tyr Gly Tyr Gly Gly Ser Glu Asp Ser Ser Asn
 340 345 350

<210> 27

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide

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<400> 27
catggaggag cag

13

<210> 28
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 28
ctgctcctc

9